

1 GAATTGGCC CTCGAGGCC AGAATTGGC ACGAGGGCG CCGCCCAGGC CAGGGAGGC GCTGTGGCAT CCCGGCGTC CACCCGCCAT GGGGCTCTCC
 1 CTTAACCGG GAGCTCCGGT TCTTAAGCG TGCTTCCGGC CGGGGGTCCG GTCCGCTCTG CGACAGCGTA GGGCCCGAG GTGGGCGGTA CCCCAGGG
 Me tGlyLeuSer

101 TGGAGCCCG GACCTCCACT GCTGATGATC CTGCTACTGG TCTGTCTGG GTGGGTGCCA CTGGGAGCAG GAAACTCCCT TGCCACAGAG AACAGGTTTG
 ACCTGGGG CTGGAGGTGA CGACTACTAG GACGATGACC ACGACAGCA CACCGACGGT GAACCTTGCTC CTTTGACCAA ACCGTTGCTC TTGTCAC
 5 TrpSerProA rgProProle uLeuMetIle LeuLeuLeuV alleuSerle utrPleuPro LeuGlyAlaL 1yAsnSerLe uAlaThrGlu AsnArgPheVal

201 TGAACAGCTG TACCCAGGGCC AGAAAGAAT GCGAGGGCTAA TCCCCGCTTG AAGGGCTGC ACCAGGACCT GGGCTCCTGC ACCTCCAGTT TAAGCAGGCC
 ACTTGTCGAC ATGGTCCGG TCTTCTTAA CGCTTCCGATT AGGGCAACG TTCCGACGG TGTCGTCGAA CCCGAGGACG TGAGGCTCAA ATTGTCGG
 39 AsnSerCys sThrGlnAla ArgLysLysCys YsGlnAlaAs nProAlaCys LysAlaAlaT yrGlnHisLe ugLyserCys ThrSerSerL euSerArgPro

301 GCTGCCCTTA GAGGAGCTTA CCTAGTCTG AGACTGCTTA GAGGCCAG AACAACTCAG GAAACAGCTC CTGATAGACT GCAGGTGCTA TCGGGCCATA CGAGGTGCTA
 CGACGGGAT CCTCCAGAC GGTACAGACG TCTGACGGAT CTCCGTCGTC TTGTCAGTC CTGTCGAGA GACTATCTGA CGTCCACGGT AGCCGGTAC
 72 LeuProLeu GluGluSerA IaMetSerAl aaspCysLeu GluAlaAlaG lugInLeuAr gasnSerSer LeuIleAspc ysArgCysHI sArgArgMet

401 AAGCACCAAG CTACCTGTCT GGACATTAT TGGAACCGGTC ACCCTGGCCG AAGCCCTGGT GACTACGAGT TGGATGCTCT ACCCTATGAA GACACAGTGA
 TTCGTTGGTTC GATGGACAGA CCTGTAATA ACCTGGCAAG TGGACGGGC TTGGAAACCA CTGATGCTCA ACCTACAGAG TGGGATACTT CTGTCGTC
 105 LysHisGlnA IaThrCysLe uAspIleYr TrpThrValH iProAlaAla gSerLeuGly AspTrpGluIle uAspPheValIle rProTrpGlu AspThrValHr

501 CCAGCAAMC CTGGAAAATG AATCTTAGCA AGTTGAACAT GCTCAAACCA GACTCGGACC TCTGCCTCAA ATTGCTATG CTGTCGACTC TTACAGACAA
 GGTGTTGG GACCTTTAC TTAGAAATGT TCAACTTGTA GAGTTGGT CTGAGCTGG AGACGGAGT TAAACGATAAC GACACATGAG AAGTGTGTT
 139 SerLysPr oTrpLysMet AsnLeuAsnMe tLeuLysPro AspSerAspL euCysLeuL ySheAlaMet LeuCystHRL euHisAspLys

601 GTGTGACCGC CCTACGGGA GGCATGCTCA GGGATCCGCT GCCAGGCCA CCTCTGCCA GCCCAGCTGC GCTCCTCTT TGAGAAGGCA
 CACACTGGCG GACGGTTCC GGATGCCCT CCGTAGCAGT CCCTAGGCCA CGGTGCCGGT GGAGACGGAT CGGGTCGACG CGAGGAAGAA ACTCTCCGT
 172 CysAsparg LeuArgLysA 1aTyRGLyG1 uAlaCysSer GlylLeaRgC ysGlnArgHi sLeuCysLeu AlagInLeuA rgSerPhePh eGluLysAla

701 GCAGAGTCCC ACGGTCAGGG TCTGCTGTG TGTCCCTGTG CACCAAGAGA TCGGGGCTGT GGGGAGGGC GGGGAAACAC CATGGCCCC
 CGTCTCAGGG TGCGAGTCCC AGACGACAGAC ACAGGGACAC GTGGCTCTCTCT ACGGCCGACA CCCCCTGGCG CGCATTGTCG GTAGGGGG
 205 AlaGluSerH isAlaGlnG1 yLeuLeuL CysProCysA 1aProGluAs pAlaGlyCys GlyGluLysA rgArgAsnTh rileAlaPro SerCysAlaLeu

801 TGCCTCTGT AACCCCCAAT TGCCTGGATC TGCGGAGCTT GACGATCAGC CCTGATGGAC TTCCAGACCC ACTGTOATCC
 ACGGAAACA TTGGGGTTA ACGGACCTAG ACGCCTCGAA GACGGCAGC CTGGAAACA CGCTCTAGTC GGACTACCTG AAGGTCTGGG TGACAGTAGG
 239 ProSerVa 1ThrProAsn CysLeuAspL euArgSerPh ecysArgAla AspProLeuC ysArgSerAr gLeuMetAsp PheGlnThrH isCysHisPro

901 TATGGACATC CTTGGGACTT GTGCAACTGA GCAGTCCAGA TGTCTGGGG CATACTGGG GCTGATTGGG ACTGCCATGA CCCAAACT CATCAGCAAG
 ATACCTGTAG GAACCCGAA CACGTTGACT CGTCAGGTCT ACAGAGGCC GTATGGACCC CGACTAACCC TGACGGTACT GGCTCTGGAA GTAGTCGTT
 272 MetAspIle LeuGlyThrC ysAlaThrG1 uGlnSerArg CysLeuArgA 1aTyRLeuG1 yLeuIleGly ThrAlaMetT hrProAsnPh eileSerLys

FIG. 1A

1001 GTCAACACTA CTGTCGCCTT AAGCTGCACC TGGCGAGGCA GCGGCAACCT ACAGGACGAG TGTGAACAGC TGAAAGGTC CTTCTCCAG AACCCCTGCC
 CAGTTGTGAT GACAACGGA TTGACGTCGG AGCGGTCCTCGT CGGCCGTTGGA TGTCTCGTC ACACATTGTCG ACCTTTCCAG GAAGGGGACGG
 305 ValAsnThr hrvalAlaLe userCysThr CysArgLys erglyAsnLe uGlnAspGlu CysGluGlnL euGluArgSe rPheSerGln AsnProCysLeu

1101 TCGTGAGGG CATTGAGGT AAGATGCGTT TCCACAGACA GCTCTTCTCC CAGGACTGGG CAGACTCTAC TTTTCAGTG GTGCAGGAGC AGAACAGCAA
 AGCACCTCCG GAACTACGCA TTCTACGCA AGGTGTCGT CGAGAAAGAGG GTCTGACCC GTCTGAGATG AAAAGTCAC CACGTCGTG TCTGTGTT
 339 ValGluAl aileAlaAla LysMetArgP hehisArg1 nleuPheSer GluAspTrpA laAspSerTh rPheSerVal ValGlnGln ValAsnSerAsn

1201 CCCTCTCTTG AGACTGGAGC CCAGGCTTACCATCC TTTCTCCATCC TTCCCTTGAT TCTGCTGAG ACCCTCTGGT AGCTCTGGCTT CCTCAGGGTC
 GGGACGAGC TCTGACGTC GGTCGATGG GTAAGAAAAGA AAGGGTAGG AAGGGAACTA AGACGACGTC TGGAGACCA TCGACCCAA GGAGTCCCAG
 372 ProAlaLeu ArgLeuGlnP roArgLeuPr oIleLeuSer PheSerIleL euProLeuIleL eLeuLeuGln ThrLeuTrp

1301 CTTGTCCCTC TCACCAACAC CCAGACTGAT TTGCAAGCTG ACCACCTCTT CTTGAGGGT CCGACACTT CTTCTGCTGC GCACGATGTT CGTGTGGCC

1401 AACCAACAG GCATTCCGCA GCACATCCCG TCTGCTCCAG AAGAGGTCTT AGAAGTGTAGG GCTGTGACCC TTCGATCCT GAGGGGTAG TTTCAAAACC
 TTGGTGGTC CGTAAGGGGT CGTGTAGGGC AGACGAGGTC TTCTCCAGAA TCTTCACTCC CGACACTGGG AGGGCTAGGA CTCGCGATC AAAAGTTGG

1501 TCCCTTGGCC CTGGCTCCTT CTGGCTCAGG CTGCTCCTCC TTAGGACTTT GTGGGTCCAG TTTGCTTCCAG GCTCACCTTC GCTGATTAGG GCTCACCTTC
 AGGGAAACGGG GACGAAAGGA GACGGAGTCC GACGGAGGG AAATCCTGAAA CACCCAGGTC AAAACGGAA AGCAAGACTAC CACTAATGCG CGAGTGGAGG

1601 AGGGCTTCTT CCTGTTCCC AGGACCAACCC AGGGCTAAG GAATCAGTCA TTCCCTGTTG CTTCTCAG GAAGGCAGGC TAAGGGTCT GAGGTGACTG
 TCGCGAAAGAA GGACAAAGGG TCCTGTTGGG TCTCCGATC CTTAGTCAGT AGGGACAAC GGAAGGGTC CTTCCGTCCG ATTCCAAAGA CTCCACTGAC

1701 AGAAAAATGT TTCTTGTG TGAAAGGCTG GTGCTCCAGG CTCCACGTCC CTCGAATGG AAGATAAAAA CCTGCTGGT TCTGCCAGGC
 TCTTTTACA AAGGAAACAC ACCTTCGAC CACGGGGTC GAGGTGGAGG GAGACTTACCT TTCTATTTC GGACGACAC AGAAACTGAC AGACGGTCCG

1801 AATCCCTGAAAC ATTGGGCAAT GAAGAGCTAA AGTCTTGGG TCTTGTATAA CTCCCTATTAC TGTCCTAA TTCCCTAGT CCCTGGGTC ATGATTAAC
 TAGGACTTG TAAACCCGTA CTCTCGATT TCAGAAACCC AGAACAAATT GAGGATAATG ACAGGGTTT AAGGGGATCA GGGAAACCGAG TACTAATTG

1901 ATTTTGACTT AAAAAAAA AAAAAAAA AAAAAA
 TAAACTGAA TTTTTTTTT TTTTTTTTTT TTTTT

FIG. 1B

REPLACEMENT SHEET

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REPLACEMENT SHEET

FIG. 3

hGFRa3 1 M V R P [N P R P L P P V V L M L L] L P P S P L P L A G D P L P T E S R L M N S C L Q A R K
mGFRa3 1 - M G L S W S P R P P L L M I L L V L S L W . L P L G A G N S L A T E N R F V N S C T Q A R K

hGFRa3 51 C Q A D P T C S A A Y H H L D S C T S S I S T P L P S E E P S V P A D C L E A A Q Q L R N S S L I G
mGFRa3 48 C E A N P A C K A A Y Q H L G S C T S S L S R P L P L E E S A M S A D C L E A A E Q L R N S S L I D

hGFRa3 101 C M C H A R R M K N Q V A C L D I Y W T V H H A R S L G N Y E L D V S P Y E D T V T S K P W K M N L S
mGFRa3 98 C R C H A R R M K H Q A T C L D I Y W T V H H P A R S L G D Y E L D V S P Y E D T V T S K P W K M N L S

hGFRa3 151 K L N M L K P D S D L C L K F A M L C T L N D K C D R L R K A Y G E A C S G P H C Q R H V C L R Q L
mGFRa3 148 K L N M L K P D S D L C L K F A M L C T L H D K C D R L R K A Y G E A C S G I R C Q R H V C L A Q L

hGFRa3 201 L T F F E K A A E P H A Q G L L L C P C A P N D R G C G E R R R N T I A P N C A L P P V A P N C L E
mGFRa3 198 R S F F E K A A E S H A Q G L L L C P C A P E D A G C G E R R R N T I A P S C A L P S V T P N C L D

hGFRa3 251 L R R L C F S D P L C R S R L V D F Q T H C H P M D I L G T C A T E Q S R C L R A Y L G L I G T A M
mGFRa3 248 L R S F C R A D P L C R S R L M D F Q T H C H P M D I L G T C A T E Q S R C L R A Y L G L I G T A M

hGFRa3 301 T P N F V S N V N T S V A L S C T C R G S G N L Q E E C E M E G F F S H N P C L T E A I A A K M A
mGFRa3 298 T P N F I S K V N T T V A L S C T C R G S G N L Q D E C E Q L E R S F S Q N P C L V E A I A A K M A

hGFRa3 351 F H S Q L F S Q D W P H P T F A Y M A H Q N E N P A V R P Q P W V P S L F S C T P L I L L S L W
mGFRa3 348 F H R Q L F S Q D W A D S T F S V V Q Q Q N S N P A L R L Q P R L P I L S F S I P L I L L Q T L W

REPLACEMENT SHEET

48613	1	MVRPLNPRPLPPVVLMLLPLLPSPLPLAAGDPPLPTESRLMNSCLQARK	
48614	1	MVRPLNPRPLPPVVLMLLPLLPSPLPLAAGDPPLPTESRLMNSCLQARK	
48613	51	CQADPTCSAAYHHLDSCSTSISTPLPSEEPSVPADCLEAAQQLRNSSLIG	
48614	51	CQADPTCSAAYHHLDSCSTSISTPLPSEEPSVPADCLEAAQQLRNSSLIG	
48613	101	CMCHRRMKNQVACLDIYWTVHRAARSLGNYELDVSPYEDTVTSPWKMNL	
48614	101	CMCHRRMKNQVACLDIYWTVHRAARSLGNYELDVSPYEDTVTSPWKMNL	
48613	151	KLNMLKPDSDLCLKFAMLCTLNDKCDRRLKAYGEACSGPHCQRHVCLRQL	
48614	127	DSDLCLKFAMLCTLNDKCDRRLKAYGEACSGPHCQRHVCLRQL	
48613	201	LTFEEKAEEPHAQGLLCPCCAPNDRGCGGERRNTIAPNCALPPVAPNCLE	
48614	170	LTFEEKAEEPHAQGLLCPCCAPNDRGCGGERRNTIAPNCALPPVAPNCLE	
48613	251	LRRLCFSDDPLCRSRLVDFQTHCHPMMDILGTCATEQSRCCLRAYLGLIGTAM	
48614	220	LRRLCFSDDPLCRSRLVDFQTHCHPMMDILGTCATEQSRCCLRAYLGLIGTAM	
48613	301	TPNFVSVNVNTSVALSCTCRGSGNLQEECCEMLEGFFSHNPCLTEIAAKMR	
48614	270	TPNFVSVNVNTSVALSCTCRGSGNLQEECCEMLEGFFSHNPCLTEIAAKMR	
48613	351	FHSQLFSSQDWPHPTFAVMMAHQENPAVRPQPWSLFSCTLPLLILLSLW	
48614	320	FHSQLFSSQDWPHPTFAVMMAHQENPAVRPQPWSLFSCTLPLLILLSLW	

FIG. 4

REPLACEMENT SHEET

DNA48613.orf	1	A T G G T G C G C C C T G A A C C C G G A C C G C T G C C G C G T A G T C C T G A T G T T
GENFRA1.orf	1
GENFRA2.orf	1
DNA48613.orf	51	G C T G C T G C T G C C G C G C G C G C T G C G C C T C G C A G C C G G A G A C C C C
GENFRA1.orf	6	C C T G G C G A C C C T G T A C T T C G C G C T G C C G C T C T T G C T G T C G G
GENFRA2.orf	39	A G A C G A C C C T C C G C T T T G G C A G C C C T C T G C A G G C C C G
DNA48613.orf	101	T T C C C A C A G A A A G C C G A C T C A T G A A C A G C G C T G T C T C C A G G G A A G
GENFRA1.orf	56	C C G A A G T G A G G G G G G A G A C C G C C T G G A I T G C G G A C C G A G T C A G
GENFRA2.orf	89	A G C T C C A C G G C T G C G C C C C C C A G T G G A C T G T G A C T G T G G C C A A T G A G C T G
DNA48613.orf	151	T G C C A G G C T G A T C C A C C T G C A G T G C T G C C T A C C A C C T G A T T C C T G
GENFRA1.orf	106	T G C C T G A A G G A G G C A G G C T G C A G G A C C A A G T A C C G C A C G T A G T G
GENFRA2.orf	139	T G T G C C G C G A T C C A A C T G C A G G C T C T G G C A C T G T G G C A G T G
DNA48613.orf	201	C A C C T C T A G C A T A A G C A C C C A C T G C C C T . . . C A G A G G A G C C T T C G G T C C
GENFRA1.orf	156	C G T G G C G G C A A G G A C C A A C T T C A G G C C T G G C C T G G A G G G C C A
GENFRA2.orf	189	C C T G C A G G C C G C G A C C G C A A C A C C A T G C . . . T G G C C A
DNA48613.orf	248	C T G C T G A C T G C C T G G A G G G A G C A A C T C A G G A A C A G C T C T G A T A
GENFRA1.orf	206	A G G A T G A T G C C G C A G G C C A T T G G A G G C C C T G A A G C A G A A G T C G T C T A C
GENFRA2.orf	224	A C A A A G G A G T G C C A G G C G G C C T T G G A G G T C T T G C A A G G A G G C C C G C T G T A C
DNA48613.orf	298	G G C T G C A T G C C C G C A C C G G C A T G A A G A A C C A G T G C T G C T T G G A C A T
GENFRA1.orf	256	A A C T G C C G C T G C A A G G G G G T A T G A A G A A G G A G A A G A A C T G C C T G C G C A T
GENFRA2.orf	274	G A C T G C C G C T G C A A G G G G G C A T G A A A G G A G G C T G C A G T G T C T G C A G A T
DNA48613.orf	348	C T A T T G G A C C G T C A C C G T G C C C G C A G C C T T G G A A C T A T G A G C T T G G A T G
GENFRA1.orf	306	T T A C T G G A G C A T G T A C C A G A G G C C T G C A G G G A A A T G A T C T G C G G G A T T
GENFRA2.orf	324	C T A C T G G A G C A T C C A C C T G G G G C T G A C C G A G G G T G A G G A G T T C T A C G A A G

FIG. 5A

FIG. 5B

REPLACEMENT SHEET

DNA48613.orf	718	GCGCTGCC - . - GCGCTGTGGCCACTGCCCTGGAGCTTGC GG C C T C T G GDNFR1.orf	685	T CCTATGAAAGAGGGAAAGCCCACCTGTGTGTGAATTGCAAGAACCTCCTG GDNFR2.orf	724	T CCTATGAGGACAAGGAAAGCCCACCTGCCCTGGAGCTGGTGTG
DNA48613.orf	765	C TTCTCCGACCCGCTTTGCAGATCACGCCCTGGATTCAGACCCACT GDNFR1.orf	735	CAAAGACGAAATTACATCTGCAGATCTGCCCTGGGATTTTACCAACT GDNFR2.orf	774	CGGACTGACCAACCTGTGTGGTCCCCTGGACCTCCATGCCAATT
DNA48613.orf	815	GCCATCCCCATGCCATCCCTAGGAACCTGTGCAACAGGCACTGGAGA... GDNFR1.orf	785	GCCAGCCAGTCAAGGTCTGTCAGGAGCTGTCTAAAGGAAACTACGCT GDNFR2.orf	824	GTCGAGCCCTCCTACCAAGACGGTACCCAGCTGGGACAAATTACAG
DNA48613.orf	862	TGTCTACCGACATACTGGGCTGATTGGGACTCATGACCCCCAA GDNFR1.orf	835	GACTGCCCTACCTCGGGCTTATTGGCACACAGTCATGACCCCCAA GDNFR2.orf	874	GCTGTCGGCTTATGCTGGCATGATTGGGTTGACATGACACCTAA
DNA48613.orf	909	CTTGTCAAGCAATGTCA - . . . - ACACAGTGTGCCCTAAGCTGCACCT GDNFR1.orf	885	CTACATGACTCCAGTA - . . . - GCCTCAGTGTGGCCCATGGTGACT GDNFR2.orf	924	CTATGTGACTCCAGGCCACTGGCATCGTGGTGTCCCCCTGGTGCAAGCT
DNA48613.orf	953	GCGAGGGCAAGTGCACCTGCAAGGAGTGTGAAATGCTGGAAAGGGTT GDNFR1.orf	929	GCAGCAACAGTGGGAAACGACCTAGAAAGAGTGCCTGAATAATTCTGAAATTTC GDNFR2.orf	974	GTCGTGGAGCAGGGAAACATGGAGGGAGTGTGAGAAAGTTCTCAAGGAGAC
DNA48613.orf	1003	TTCTCCACAAACCCCTGCCCTCAAGGCCATTGCAGCTAAGATGGGTT GDNFR1.orf	979	TTCAAGGACAATACATGTTCAAAATGCAATTCAAGGCTTGGCAATTGG GDNFR2.orf	1024	TTCAACCGAGAACCCATGCCCTGGAAAGGCCATTCCAGGGCTTGGCAACCGG

FIG. 5C

REPLACEMENT SHEET

GENERAL1.orf 1379 C A T A G

REPLACEMENT SHEET

DNA48613	1	MVRPLNPRPLPPVVLMLLLPSPPLPLAAGDPLPTESRLMNSCLOARRK
GDNFRa1	1	MFLAT--LYFAL--PLLDLSSA--EVSGGD----RL--DCVKASDQ
GDNFRa2	1	MILANVFCLFFFDETSLRSLASPS--SLLQGPELHGWRPPV--DCVRANEL
DNA48613	51	CQADPTCSAAHYHLDSCCTSSISITPLP-SEEPSVPADCLEAAQQLRNSSLI
GDNFRa1	36	CLKEQS CSTKYRTL RQC VAGKETNF SLASGLEAKDEC R S A M E A L K Q Q S L Y
GDNFRa2	47	CAAESNCSSR YRTL RQC LAGRDRN----TMLANKECQA ALEVLQ E S P L Y
DNA48613	100	GCMCHRRMKNQVACLDIYWTVHRARSLGNYELDVSPYEDTVTSKPWKMN L
GDNFRa1	86	NCRCKRGMKKEK NCLRIYWSMY QSL - Q GNDLLEDSPYEPVN SRLSDIFRV
GDNFRa2	92	DCRCKRGMKKELQCLQIYWSIH LGLT EGEFFYEASPYEPVTSRLSDIFRL
DNA48613	150	SKL----NMLKPDSDLCLKFAMLC TLN D KCDRLRKAYGEAC S---
GDNFRa1	135	VPFIS---VEHI--PKGNNCLDAAKACNLDDICKKYRSAYITPCTTSVS-
GDNFRa2	142	ASIFS GTGADPVVSAKS NHCLDAAKACNLNDNCKKL RSSY I SICNREISP
DNA48613	188	GPHCORHVCLRQLLTFFEKAAEPAHAGL LCP CAPNDRGCGERRRNTIA P
GDNFRa1	179	NDVCNRRKCHKALRQFFDKVPAKHSYGM LFCSC - RDI ACT TERRRQTIVP
GDNFRa2	192	TERCNRRKCHKALRQFFDRVPSEYT YRMLFCSC - QDQACAERRRQTILP
DNA48613	238	N CALPPVA-PNQCLELRRLCFSDP LCRSRLVDFQTHCHP-MDILGT CATEO
GDNFRa1	227	VCSYEEEREKPNCNLNQDSCKTNYICRSRLADFTNCQPESRSVSSCLKEN
GDNFRa2	240	SCSYEDKEKPNCNLDLRGVCRTDHLCRSRLADFHANCRA SYQTVTSCPADN
DNA48613	286	-SRCLRAYLGLIGTAMTPNFVSNV--NTSVALSCTCRGSGNLQEEC EML E
GDNFRa1	277	YADCLLAYSGLIGTVMTPNYIDSS-SLSVAPWCDCNSNGNDL EECLKFL
GDNFRa2	290	YQACLGSYAGMIGFD MTPNVDSSPTGIVVSPWCSCRGSGNME EEC EKFL
DNA48613	333	GFFSHNPCLTEAIAA-----KMRFHSQLFS
GDNFRa1	325	NFFKDNTCLKNAIQAFGNGSDVTWQPAFPVQTTTATT TALRVKNKPLLG
GDNFRa2	340	RDFTEENPCLRN AIQAFGNGTDVN VSPKGPSFOATQAPRVEKTPSLPDDLS
DNA48613	358	Q-----DWPHPTFAVMAHQNE NPA VRPQ-----
GDNFRa1	375	PAGSENEIPTHVLPPCANLQAOQKLKSNVSGNTHLCISNGNYEKEGLGASS
GDNFRa2	390	DSTS---LGTSVITTC TSVQEOGLKANNSKELSMCFT-ELTTNIIPGSN
DNA48613	381	-----PWVPSLFSC TLPLILLLSLW-----
GDNFRa1	425	HITTKSMAAPPSCG LSP LLVLVVTALSTLLSLTETS
GDNFRa2	435	KVIKPNSGPSRARPSAALT VLVSLVMLKQAL-----

FIG. 6

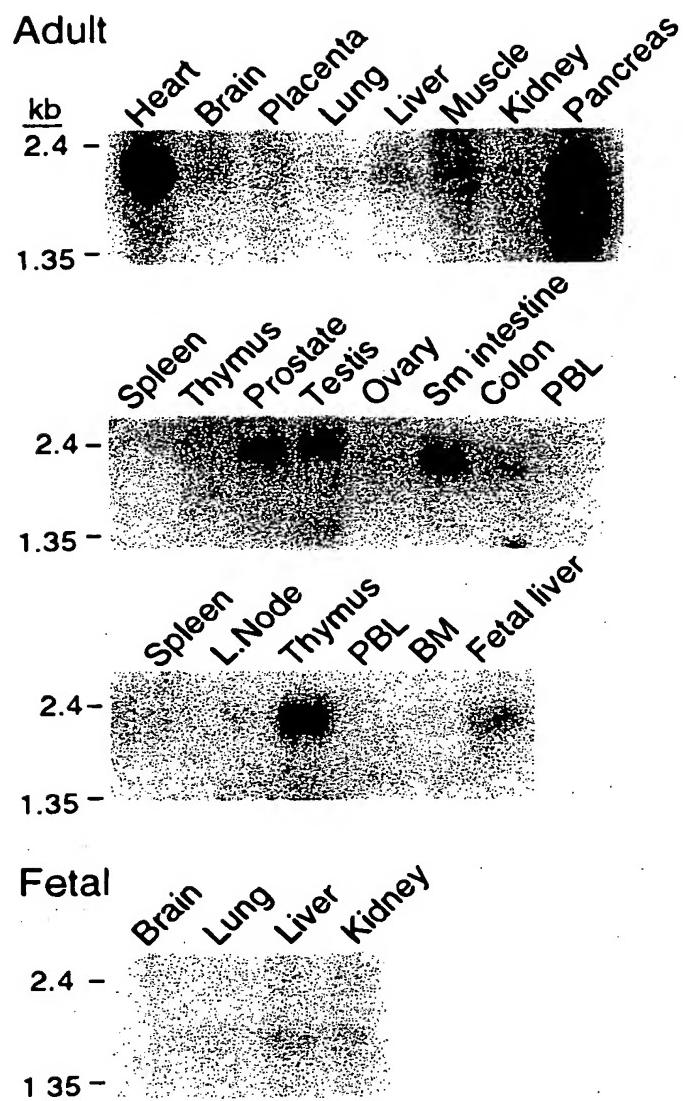
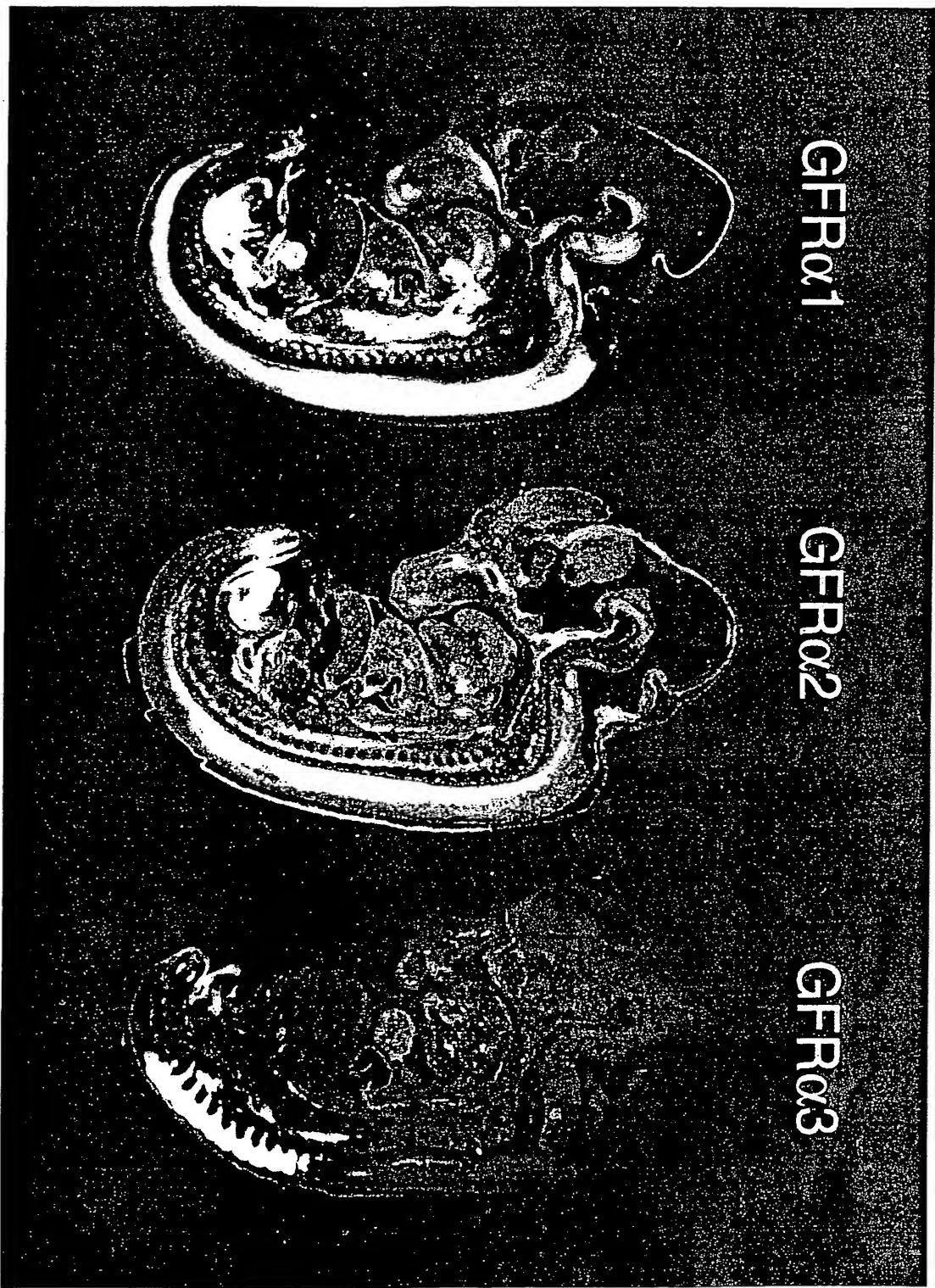


FIG. 7

REPLACEMENT SHEET

FIG. 8



Binding to Rat GFR_{a1}-IgG

FIG. 9A

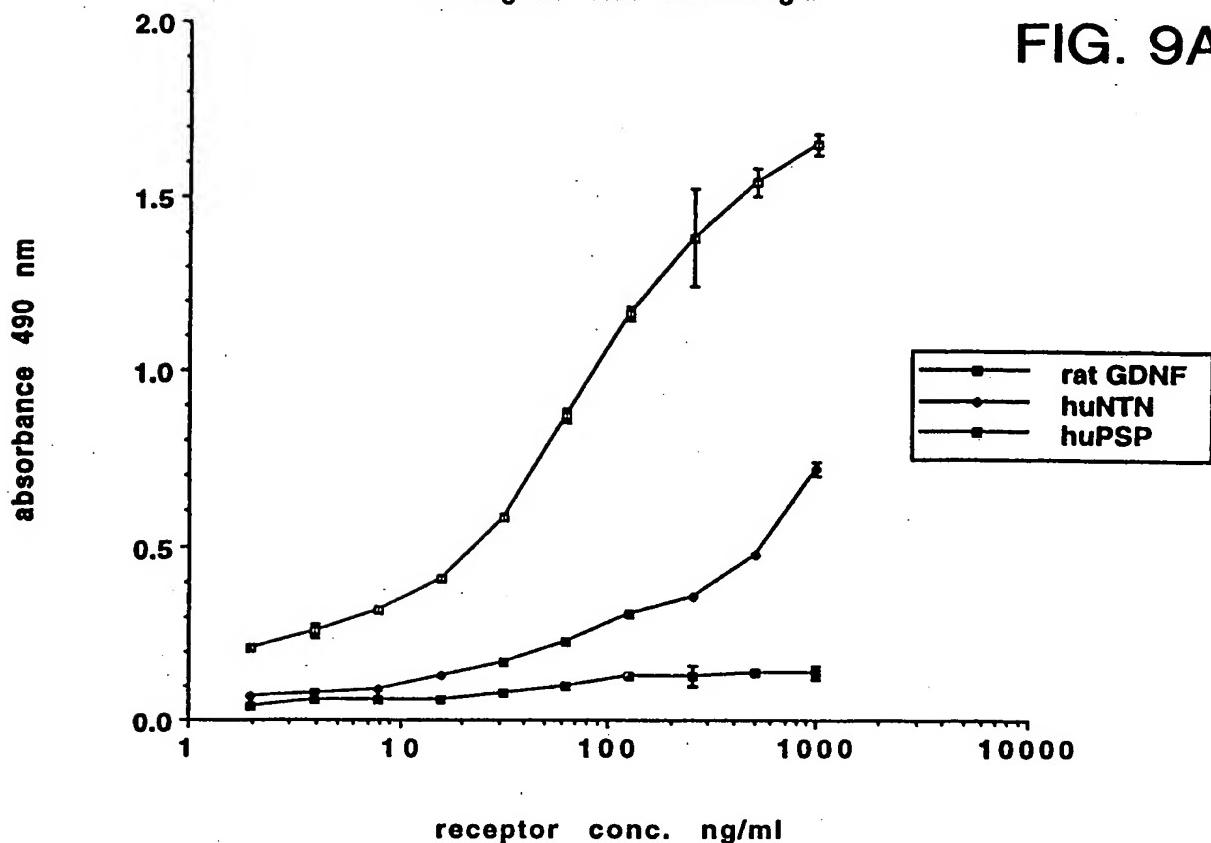
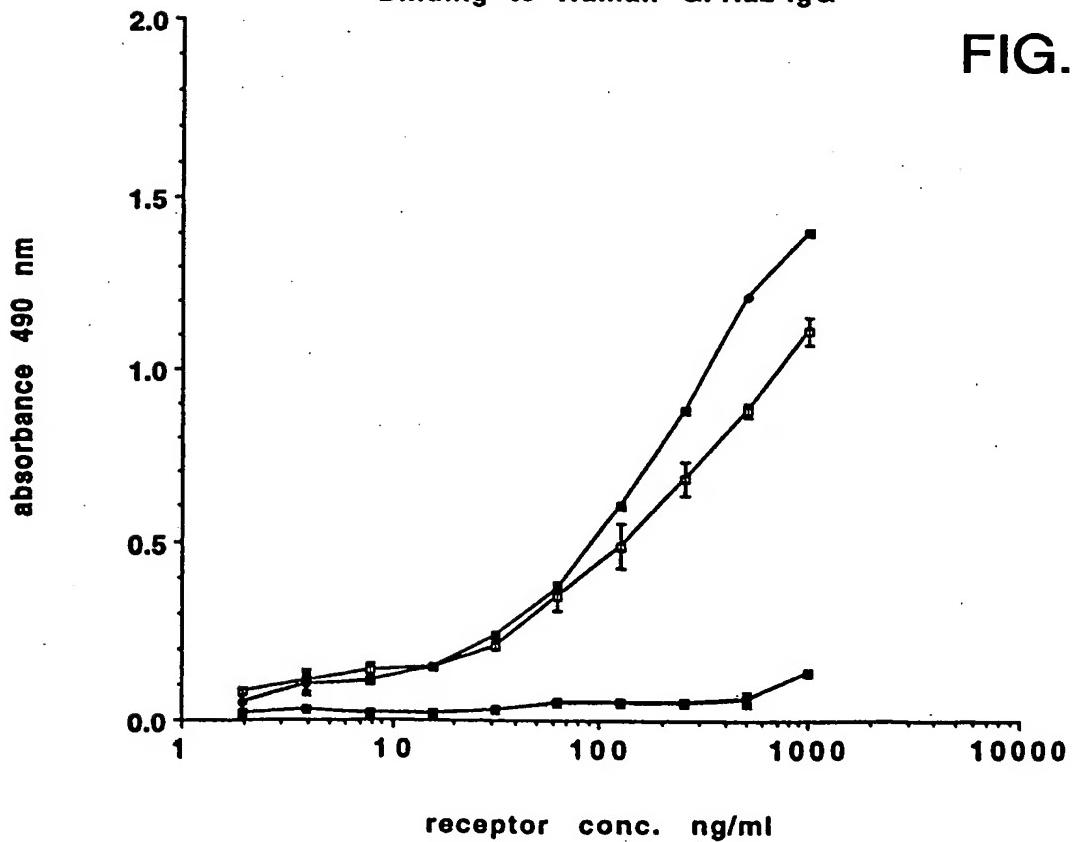
Binding to Human GFR_{a2}-IgG

FIG. 9B



REPLACEMENT SHEET

Binding to Human GFR_a3-IgG

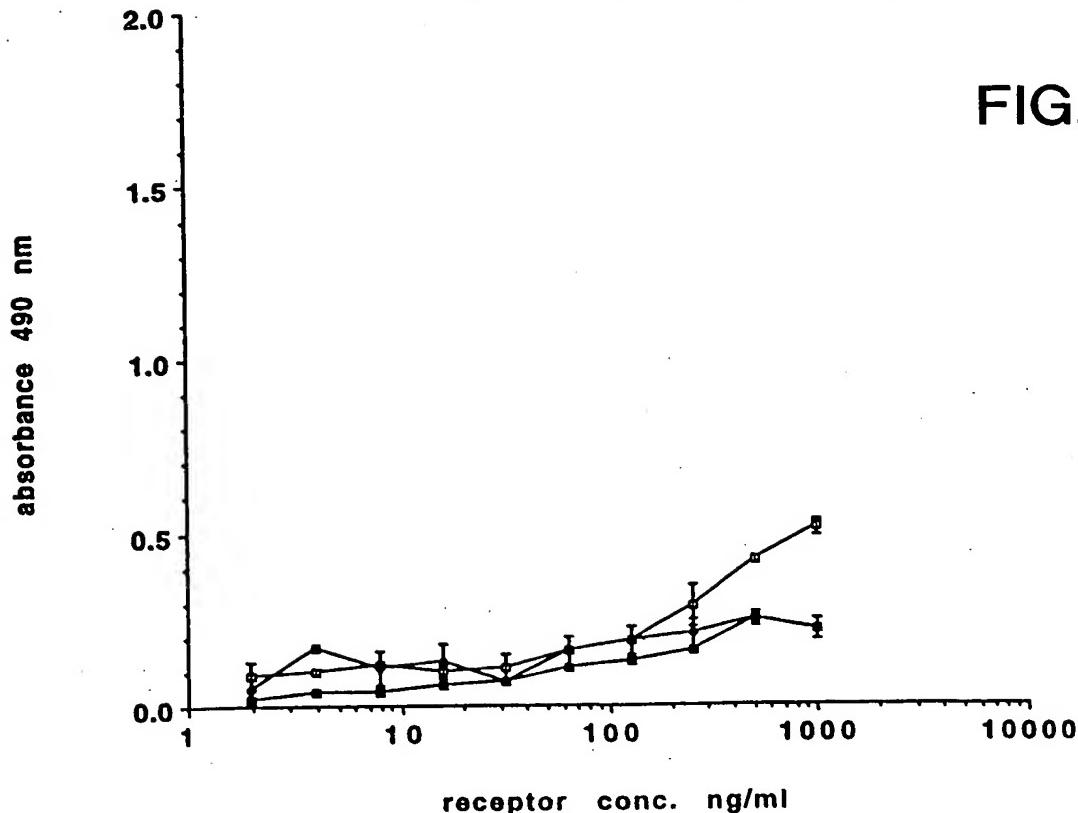


FIG. 9C

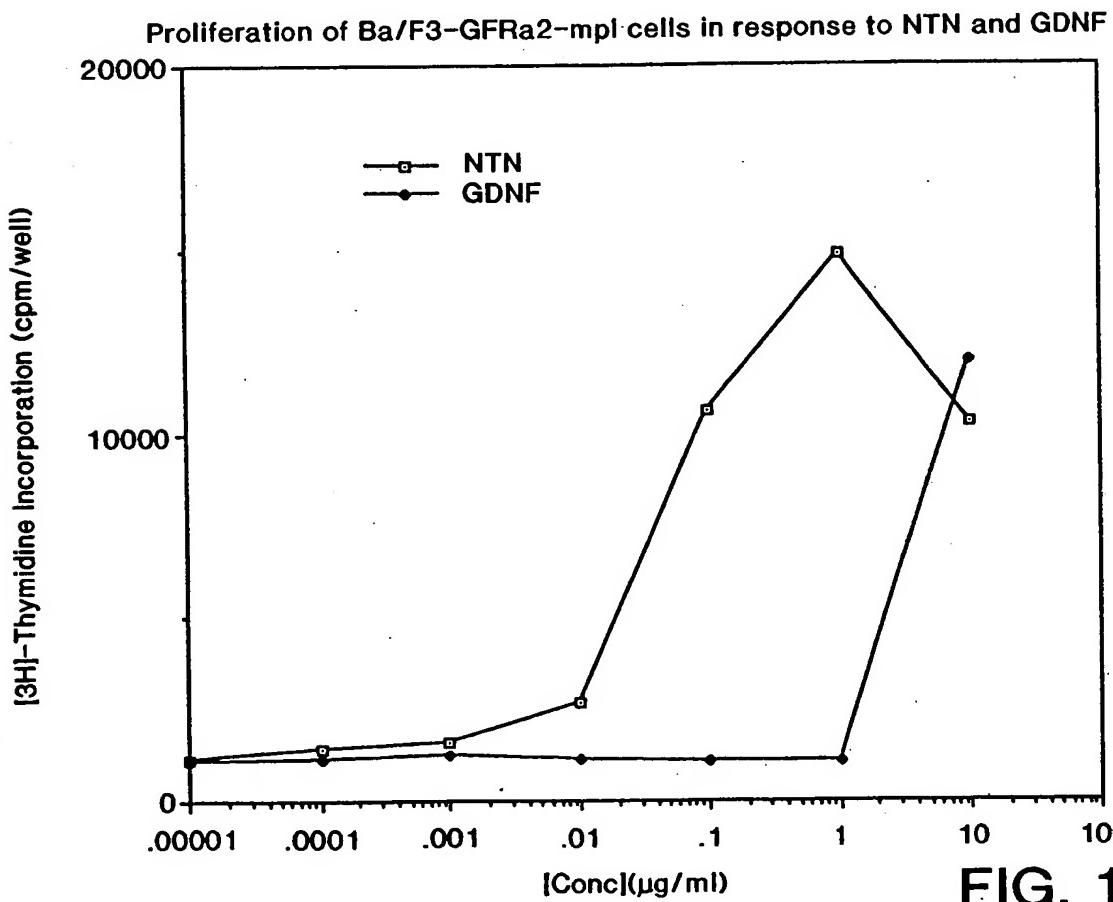


FIG. 10

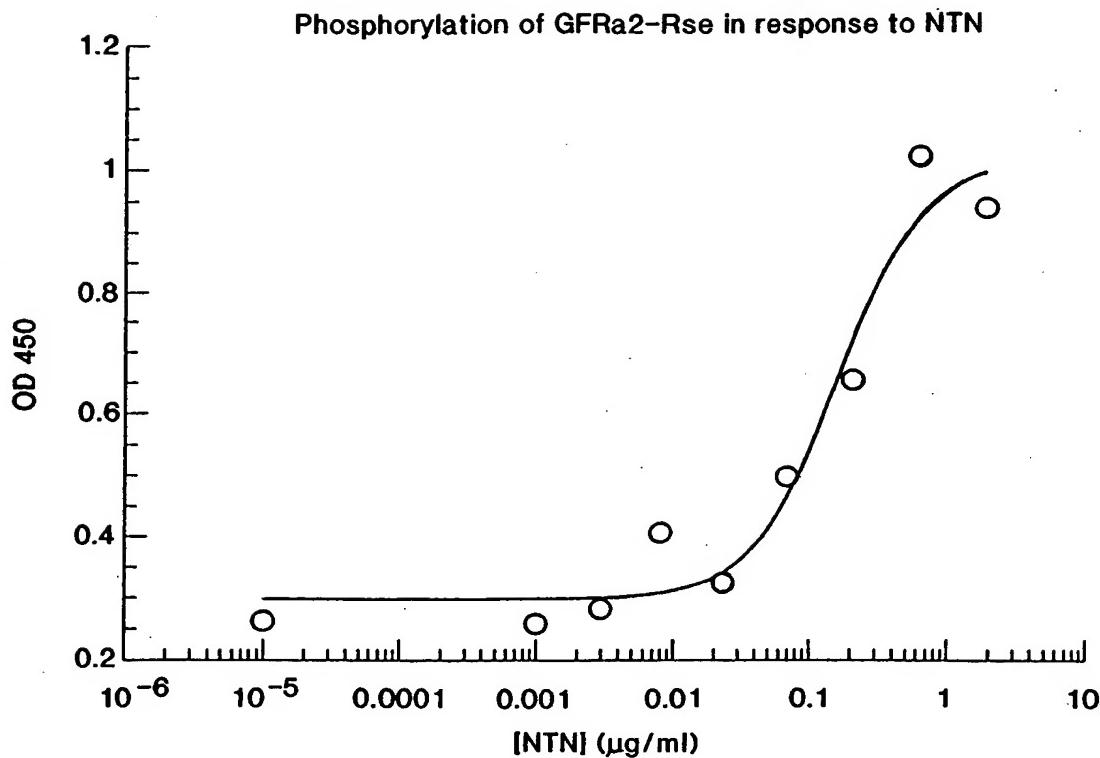


FIG. 11

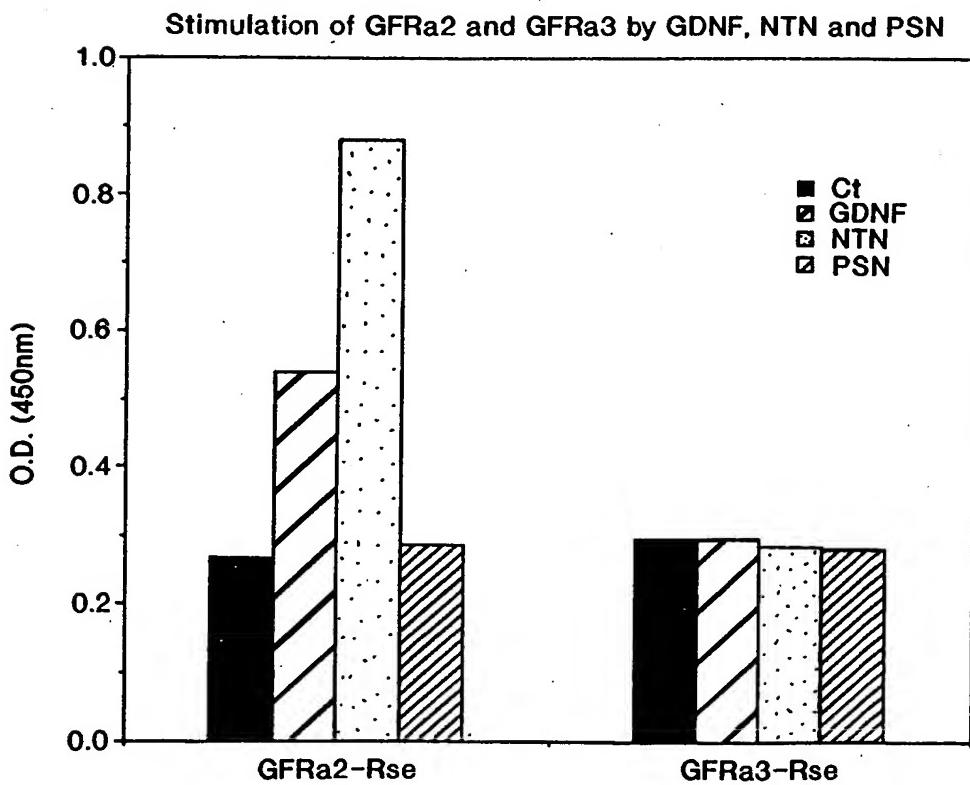


FIG. 12

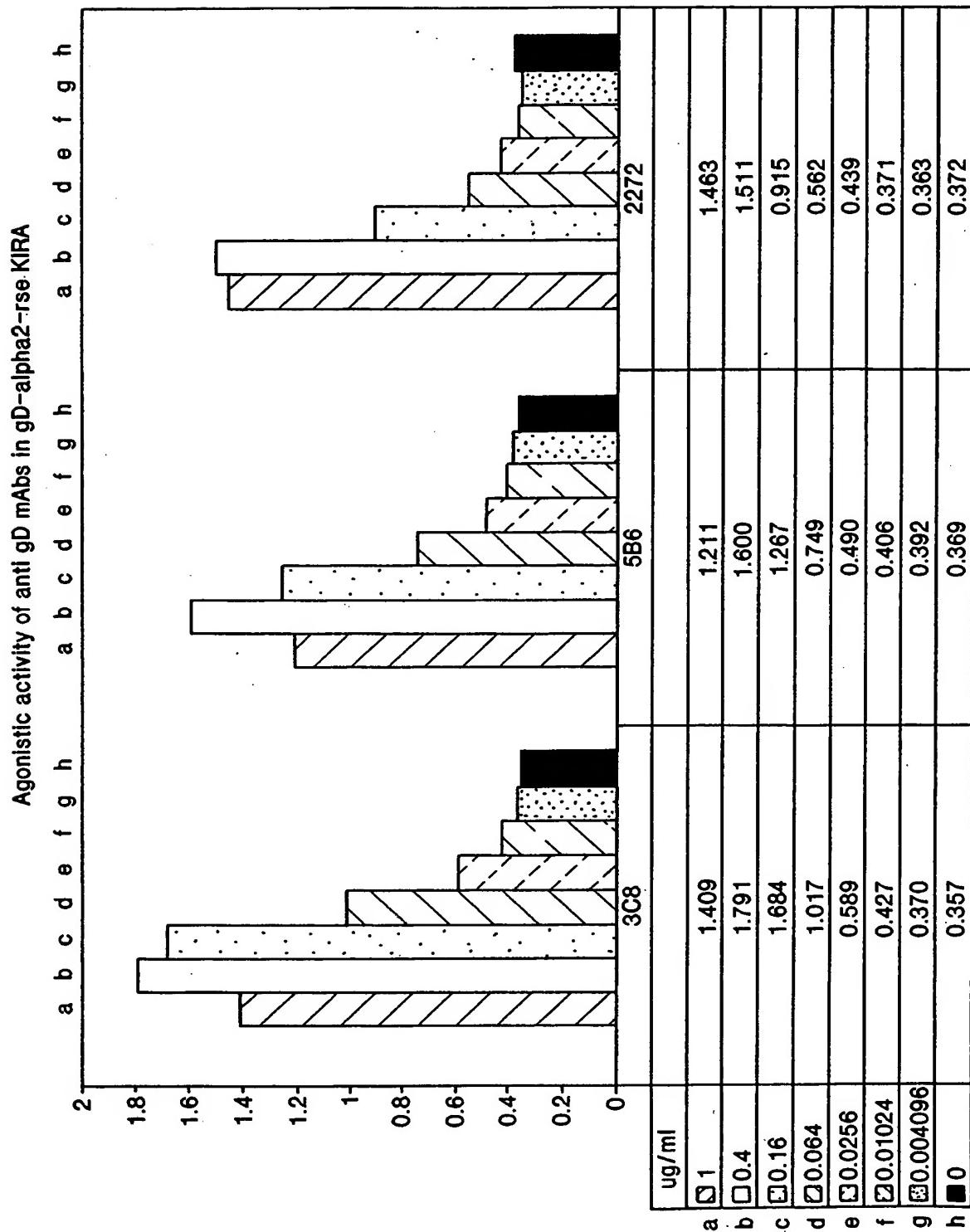


FIG. 13

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